

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:48:56

INPUT SET: S2395.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

wrapped
text

SEQUENCE LISTING

(1) General Information:

(i) APPLICANTS:

↑ start response on this line
Hauptmann, R.
Falkner, E.
Bodo, G.
VoÄ, T.
Maurer- Fogy, I.

(ii) TITLE OF INVENTION: Process for Preparing and Purifying
alpha-Interferon

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox
(B) STREET: 1100 New York Avenue, Suite 600
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: U.S.A.
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: herewith
(C) CLASSIFICATION:

delete space

Information:

(viii) ATTORNEY/AGENT NUMBER:

(A) NAME: Esmond, Robert W. RWE/EG
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0652.1350000

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 371-2600
(B) TELEFAX: (202) 371-2540

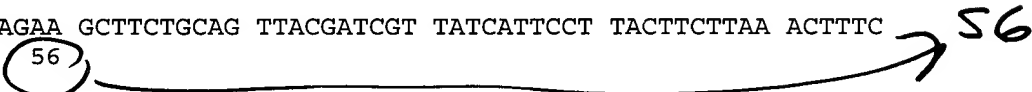
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PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:05

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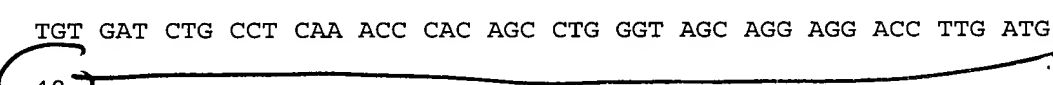
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ERRORED SEQUENCES FOLLOW:

61 (2) INFORMATION FOR SEQ ID NO: 2:
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63 (i) SEQUENCE CHARACTERISTICS:
--> 64 (A) LENGTH: 56 base pairs
65 (B) TYPE: nucleic acid
66 (C) STRANDEDNESS: both
67 (D) TOPOLOGY: unknown
68
69 (ii) MOLECULE TYPE: cDNA
70
71
72
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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75 GACTTCAGAA GCTTCTGCAG TTACGATCGT TATCATTCCT TACTTCTTAA ACTTTC
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77



156 (2) INFORMATION FOR SEQ ID NO: 6:
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158 (i) SEQUENCE CHARACTERISTICS:
--> 159 (A) LENGTH: 495 base pairs
160 (B) TYPE: nucleic acid
161 (C) STRANDEDNESS: both
162 (D) TOPOLOGY: unknown
163
164 (ii) MOLECULE TYPE: cDNA
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167 (ix) FEATURE:
168 (A) NAME/KEY: CDS
169 (B) LOCATION: 1..495
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176 48
177 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
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180 CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC TGC TTG AAG GAC
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182 96
183 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp



48
etc...
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94
TIME: 10:49:13

INPUT SET: S2395.raw

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192 AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC CAG CAG ATC TTC
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194 192
195 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
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200 240
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204 CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG AAT GAC CTG GAA
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206 288
207 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
208      85                90                95
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210 GCC TGT GTG ATA CAG GGG GTG GGG GTG ACA GAG ACT CCC CTG ATG AAG
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212 336
213 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
214      100                105                110
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216 GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA AGA ATC ACT CTC
217
218 384
219 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
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222 TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG GAG GTT GTC AGA
223
224 432
225 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
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228 GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC TTG CAA GAA AGT
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230 480
231 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
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234 TTA AGA AGT AAG GAA
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:21

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284 (2) INFORMATION FOR SEQ ID NO: 8:
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286 (i) SEQUENCE CHARACTERISTICS:
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288 (B) TYPE: nucleic acid
289 (C) STRANDEDNESS: both
290 (D) TOPOLOGY: unknown
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292 (ii) MOLECULE TYPE: cDNA
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294
295
296 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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298 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA
--> 299 CCAACAGCGG 60
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301 TTGATTGATC AGGTAGAGGG GCGCTGTAC GAGGTAAAGC CCGATGCCAG
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303 120
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305 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
306 TCGTCAGTAA
307 180
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309 AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
310 TAGTCGCTTT
311 240
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313 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GGTGAGGTG ATTTTATGAA
314 AAAGAATATC
315 300
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329 TTTGGCAACC AGTTCCAAAA GGCTGAAACC ATCCCTGTCC TCCATGAGAT
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:30

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334 CCTCCTAGAC
335 600
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338 GATACAGGGG
339 660
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341 GTGGGGGTGA CAGAGACTCC CCTGATGAAG GAGGACTCCA TTCTGGCTGT
342 GAGGAAATAC
343 720
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345 TTCCAAAGAA TCACTCTCTA TCTGAAAGAG AAGAAATACA GCCCTTGTGC
346 CTGGGAGGTT
347 780
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349 GTCAGAGCAG AAATCATGAG ATCTTTTTTCT TTGTCAACAA ACTTGCAAGA
350 AAGTTTAAGA
351 840
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353 AGTAAGGAAT GATAACGATC GTAACGTCA
354 869
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356 (2) INFORMATION FOR SEQ ID NO: 9:
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358 (i) SEQUENCE CHARACTERISTICS:
--> 359 (A) LENGTH: 1177 base pairs
360 (B) TYPE: nucleic acid
361 (C) STRANDEDNESS: both
362 (D) TOPOLOGY: unknown
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364 (ii) MOLECULE TYPE: cDNA
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366
367 (ix) FEATURE:
368 (A) NAME/KEY: CDS
369 (B) LOCATION: 286..873
370 (D) OTHER INFORMATION: /function= "Cytokine"
371 /product= "Interferon-omega"
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373 (ix) FEATURE:
374 (A) NAME/KEY: mat_peptide
375 (B) LOCATION: 355..873
376 (D) OTHER INFORMATION: /function= "Cytokine"
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379 (ix) FEATURE:
380 (A) NAME/KEY: sig_peptide
381 (B) LOCATION: 286..354
382 (D) OTHER INFORMATION: /product= "ST II Leader"
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

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392      CATTCTGAC
393      120
394
395      GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
396      TCGTCAGTAA
397      180
398
399      AAAGTTAATC TTTTCAACAG CTGTCATAAA GTTGTCACGG CCGAGACTTA
400      TAGTCGCTTT
401      240
402
403      GTTTTTATTT TTTAATGTAT TTGCTCGAGA GTTTGAGGTG ATTTT ATG AAA AAG
404
405      294
406
407
408
409      AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
410      342
411      Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
412      -20          -15          -10          -5
413
414      AAT GCC TAT GCA TGT GAT CTG CCT CAG AAC CAT GGC CTA CTT AGC AGG
415
416      390
417      Asn Ala Tyr Ala Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg
418              1          5          10
419
420      AAC ACC TTG GTG CTT CTG CAC CAA ATG AGG AGA ATC TCC CCT TTC TTG
421
422      438
423      Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu
424              15          20          25
425
426      TGT CTC AAG GAC AGA AGA GAC TTC AGG TTC CCC CAG GAG ATG GTA AAA
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428      486
429      Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys
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431
432      GGG AGC CAG TTG CAG AAG GCC CAT GTC ATG TCT GTC CTC CAT GAG ATG
433
434      534
435      Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met
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437

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:48

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442 65 70 75
443
444 TGG AAC ATG ACC CTC CTA GAC CAA CTC CAC ACT GGA CTT CAT CAG CAA
445
446 630
447 Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln
448 80 85 90
449
450 CTG CAA CAC CTG GAG ACC TGC TTG CTG CAG GTA GTG GGA GAA GGA GAA
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452 678
453 Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu
454 95 100 105
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456 TCT GCT GGG GCA ATT AGC AGC CCT GCA CTG ACC TTG AGG AGG TAC TTC
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458 726
459 Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe
460 110 115 120
461
462 CAG GGA ATC CGT GTC TAC CTG AAA GAG AAG AAA TAC AGC GAC TGT GCC
463
464 774
465 Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala
466 125 130 135 140
467
468 TGG GAA GTT GTC AGA ATG GAA ATC ATG AAA TCC TTG TTC TTA TCA ACA
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470 822
471 Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr
472 145 150 155
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474 AAC ATG CAA GAA AGA CTG AGA AGT AAA GAT AGA GAC CTG GGC TCA TCT
475
476 870
477 Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser
478 160 165 170
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480 TGAAATGATT CTCATTGATT AATTTGCCAT ATAACACTTG CACATGTGAC
481 TCTGGTCAAT
482 930
483
484 TCAAAAGACT CTTATTTTCGG CTTTAATCAC AGAATTGACT GAATTAGTTC
485 TGCAAATACT
486 990
487
488 TTGTCGGTAT ATTAAGCCAG TATATGTTAA AAAGACTTAG GTTCAGGGGC
489 ATCAGTCCCT
490 1050

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:49:57

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492 AAGATGTTAT TTATTTTAC TCATTATTT ATTCTTACAT TTTATCATAT
493 TTATACTATT
494 1110
495
496 TATATTCTTA TATAACAAAT GTTTCCTTT ACATTGTATT AAGATAACAA
497 AACATGTTCA
498 1170
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500 GGATCCA
501 1177
502

553 (2) INFORMATION FOR SEQ ID NO: 11:
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555 (i) SEQUENCE CHARACTERISTICS:
--> 556 (A) LENGTH: 879 base pairs
557 (B) TYPE: nucleic acid
558 (C) STRANDEDNESS: both
559 (D) TOPOLOGY: unknown
560
561 (ii) MOLECULE TYPE: cDNA
562
563
564
565 (ix) FEATURE:
566 (A) NAME/KEY: CDS
567 (B) LOCATION: 286..852
568
569 (ix) FEATURE:
570 (A) NAME/KEY: mat_peptide
571 (B) LOCATION: 355..852
572 (D) OTHER INFORMATION: /function= "Cytokine"
573 /product= "Interferon-alpha-2c"
574
575 (ix) FEATURE:
576 (A) NAME/KEY: sig_peptide
577 (B) LOCATION: 286..354
578 (D) OTHER INFORMATION: /product= "ST II Leader"
579
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581 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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583 GAATTCGAGA TTATCGTCAC TGCAATGCTT CGCAATATGG CGCAAAATGA
584 CCAACAGCGG
585 60
586
587 TTGATTGATC AGGTAGAGGG GGCCTGTAC GAGGTAAAGC CCGATGCCAG
588 CATTCTGAC
589 120
590
591 GACGATACGG AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC
592 TCGTCAGTAA

RAW SEQUENCE LISTING PATENT APPLICATION US/08/249,671

DATE: 06/16/94
TIME: 10:50:05

INPUT SET: S2395.raw

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599 GTTTTTATTT TTTAATGTAT TTGCTCGAGA GTTTGAGGTG ATTTT ATG AAA AAG
600
601 294
602
603 Met Lys Lys
604 -23
605 AAT ATC GCA TTT CTT CTT GCA TCT ATG TTC GTT TTT TCT ATT GCT ACA
606 342
607 Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser Ile Ala Thr
608 -20 -15 -10 -5
609
610 AAT GCC TAT GCA TGT GAT CTG CCT CAA ACC CAC AGC CTG GGT AGC AGG
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612 390
613 Asn Ala Tyr Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg
614 1 5 10
615
616 AGG ACC TTG ATG CTC CTG GCA CAG ATG AGG AGA ATC TCT CTT TTC TCC
617
618 438
619 Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser
620 15 20 25
621
622 TGC TTG AAG GAC AGA CGT GAC TTT GGA TTT CCC CAG GAG GAG TTT GGC
623
624 486
625 Cys Leu Lys Asp Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly
626 30 35 40
627
628 AAC CAG TTC CAA AAG GCT GAA ACC ATC CCT GTC CTC CAT GAG ATG ATC
629
630 534
631 Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile
632 45 50 55 60
633
634 CAG CAG ATC TTC AAT CTC TTC AGC ACA AAG GAC TCA TCT GCT GCT TGG
635
636 582
637 Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp
638 65 70 75
639
640 GAT GAG ACC CTC CTA GAC AAA TTC TAC ACT GAA CTC TAC CAG CAG CTG
641
642 630
643 Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu
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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:50:14

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648 678
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650 95 100 105
651
652 CCC CTG ATG AAG GAG GAC TCC ATT CTG GCT GTG AGG AAA TAC TTC CAA
653
654 726
655 Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln
656 110 115 120
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658 AGA ATC ACT CTC TAT CTG AAA GAG AAG AAA TAC AGC CCT TGT GCC TGG
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660 774
661 Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp
662 125 130 135 140
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664 GAG GTT GTC AGA GCA GAA ATC ATG AGA TCT TTT TCT TTG TCA ACA AAC
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666 822
667 Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn
668 145 150 155
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672 869
673 Leu Gln Glu Ser Leu Arg Ser Lys Glu
674 160 165
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676 GAAGCTTAAT
677 879
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/249,671DATE: 06/16/94
TIME: 10:50:20**INPUT SET: S2395.raw**

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANTS:
36	Unknown or Misplaced Identifier	(viii) ATTORNEY/ AGENT NUMBER:
37	Unknown or Misplaced Identifier	(A) NAME: Esmond, Robert W. RWE/EG
38	Unknown or Misplaced Identifier	(B) REGISTRATION NUMBER: 32,893
39	Unknown or Misplaced Identifier	(C) REFERENCE/DOCKET NUMBER: 0652.1350000
64	Entered (56) and Calc. Seq. Length (0) differ	(A) LENGTH: 56 base pairs
159	Entered (495) and Calc. Seq. Length (0) differ	(A) LENGTH: 495 base pairs
287	Entered (869) and Calc. Seq. Length (10) differ	(A) LENGTH: 869 base pairs
299	# of Sequences for line conflicts w/ running total	CCAACAGCGG 60
359	Entered (1177) and Calc. Seq. Length (0) differ	(A) LENGTH: 1177 base pairs
556	Entered (879) and Calc. Seq. Length (0) differ	(A) LENGTH: 879 base pairs